



SEQUENCE LISTING

COPY OF PAPERS
ORIGINALLY FILED

#7

<110> OLSON, JERIC
STENCER, JEFFREY A.<120> METHODS AND COMPOSITIONS FOR STABILIZING MICROTUBULES
IN STRIATED MUSCLE CELLS

<130> MYOG:028US

<140> 09/908,988

<141> 2001-07-18

<150> 60/219,020

<151> 2000-07-18

<160> 6

<170> PatentIn Ver. 2.1

<210> 1

<211> 1431

<212> DNA

<213> Mus musculus

<220>

<221> CDS

<222> (199)..(1296)

<400> 1

aaggagtgtgta gacagagtgt ctggaaatag acaggggtga gaggagctgt taggggaagg 60
gacaggactc ttccaagagg gagcaatagc cgggatccca agaatccagt cagcctaaac 120
tgaccgagga aggggtgcaca ggcagggggag aaggccaacg acagggccac agcgaggcag 180
gctccagagc gccgcggg atg aac ttc acg gtg ggt ttc aag ccg ctg cta 231
Met Asn Phe Thr Val Gly Phe Lys Pro Leu Leu
1 5 10
ggg gat gcg cac aac atg gac aac ttg gag aag cag ctc att tgc ccc 279
Gly Asp Ala His Asn Met Asp Asn Leu Glu Lys Gln Leu Ile Cys Pro
15 20 25
atc tgc ctg gag atg ttc tcc aag ccc gtg gtg atc ttg ccc tgc caa 327
Ile Cys Leu Glu Met Phe Ser Lys Pro Val Val Ile Leu Pro Cys Gln
30 35 40
cac aac ctg tgc cgc aag tgt gcc aac gac gtc ttc cag gcc tct aat 375
His Asn Leu Cys Arg Lys Cys Ala Asn Asp Val Phe Gln Ala Ser Asn
45 50 55
cct ctg tgg caa tcc cgg ggc tcc aca acg gtg tct tca gga gga cgt 423
Pro Leu Trp Gln Ser Arg Gly Ser Thr Thr Val Ser Ser Gly Gly Arg
60 65 70 75
ttc cga tgc cca tct tgt agg cac gag gtt gtc ctg gac agg cat ggt 471

Phe	Arg	Cys	Pro	Ser	Cys	Arg	His	Glu	Val	Val	Leu	Asp	Arg	His	Gly		
				80					85						90		
gtc	tat	ggc	ctg	cag	cgg	aac	ctg	cta	gtg	gag	aac	atc	att	gac	atc	519	
Val	Tyr	Gly	Leu	Gln	Arg	Asn	Leu	Leu	Val	Glu	Asn	Ile	Ile	Asp	Ile		
			95					100					105				
tac	aag	cag	gag	tcc	tcc	cgg	cca	ctg	cac	gcc	aag	gct	gaa	cag	cac	567	
Tyr	Lys	Gln	Glu	Ser	Ser	Arg	Pro	Leu	His	Ala	Lys	Ala	Glu	Gln	His		
			110					115				120					
ctc	atg	tgt	gag	gag	cac	gag	gac	gag	aag	atc	aac	atc	tac	tgc	ctg	615	
Leu	Met	Cys	Glu	Glu	His	Glu	Asp	Glu	Lys	Ile	Asn	Ile	Tyr	Cys	Leu		
			125				130				135						
agc	tgc	gag	gtg	ccc	acc	tgc	tct	ctc	tgc	aag	gtt	ttc	ggc	gcc	cac	663	
Ser	Cys	Glu	Val	Pro	Thr	Cys	Ser	Leu	Cys	Lys	Val	Phe	Gly	Ala	His		
						145				150					155		
aag	gac	tgt	gag	gtg	gcc	cct	ctg	ccc	acc	att	tac	aaa	cgc	cag	aag	711	
Lys	Asp	Cys	Glu	Val	Ala	Pro	Leu	Pro	Thr	Ile	Tyr	Lys	Arg	Gln	Lys		
				160					165					170			
agt	gag	ctg	agc	gat	ggc	atc	gcg	atg	ctg	gtg	gcg	ggc	aat	gac	cgt	759	
Ser	Glu	Leu	Ser	Asp	Gly	Ile	Ala	Met	Leu	Val	Ala	Gly	Asn	Asp	Arg		
			175					180					185				
gtg	cag	gca	gtg	atc	acc	cag	atg	gag	gag	gtg	tgc	cag	acc	att	gag	807	
Val	Gln	Ala	Val	Ile	Thr	Gln	Met	Glu	Glu	Val	Cys	Gln	Thr	Ile	Glu		
			190				195					200					
gac	aac	agc	cgc	aga	cag	aag	caa	ctg	tta	aac	cag	agg	ttc	gag	acc	855	
Asp	Asn	Ser	Arg	Arg	Gln	Lys	Gln	Leu	Leu	Asn	Gln	Arg	Phe	Glu	Thr		
			205				210				215						
ctg	tgc	gcg	gtt	ttg	gag	gag	cgc	aag	ggc	gaa	ctg	ctt	caa	gca	ctg	903	
Leu	Cys	Ala	Val	Leu	Glu	Glu	Arg	Lys	Gly	Glu	Leu	Leu	Gln	Ala	Leu		
					225					230					235		
gcc	cgg	gag	cag	gag	gag	aag	ttg	cag	cgc	gtg	cgg	ggc	ctc	atc	cgc	951	
Ala	Arg	Glu	Gln	Glu	Glu	Lys	Leu	Gln	Arg	Val	Arg	Gly	Leu	Ile	Arg		
				240					245					250			
cag	tac	gga	gac	cac	ttg	gag	ggc	tcc	tca	aag	ctg	gtg	gag	tcc	gcc	999	
Gln	Tyr	Gly	Asp	His	Leu	Glu	Gly	Ser	Ser	Lys	Leu	Val	Glu	Ser	Ala		
			255					260						265			
atc	cag	tcc	atg	gag	gag	ccg	cag	atg	gct	ctc	tac	ctc	cag	cag	gca	1047	
Ile	Gln	Ser	Met	Glu	Glu	Pro	Gln	Met	Ala	Leu	Tyr	Leu	Gln	Gln	Ala		
			270				275					280					
aag	gag	ctg	atc	aac	aag	gtc	ggg	gca	atg	tcg	aag	gtg	gag	ctg	gca	1095	
Lys	Glu	Leu	Ile	Asn	Lys	Val	Gly	Ala	Met	Ser	Lys	Val	Glu	Leu	Ala		
			285				290				295						
gga	cgg	ccg	gag	cca	ggc	tat	gag	agc	atg	gag	caa	ttc	tct	gtg	agc	1143	
Gly	Arg	Pro	Glu	Pro	Gly	Tyr	Glu	Ser	Met	Glu	Gln	Phe	Ser	Val	Ser		

300

305

310

315

gtg gag cac gtg gcc gaa atg ttg cga acc atc gac ttc cag ccg ggc 1191
 Val Glu His Val Ala Glu Met Leu Arg Thr Ile Asp Phe Gln Pro Gly
 320 325 330

gcc gct ggg gat gaa gag gat gac gac atg gct ttg gat ggg gag gag 1239
 Ala Ala Gly Asp Glu Glu Asp Asp Asp Met Ala Leu Asp Gly Glu Glu
 335 340 345

ggc aat gcg ggg ctg gag gag gag cgg ctg gac gtg cca gaa ggc tca 1287
 Gly Asn Ala Gly Leu Glu Glu Glu Arg Leu Asp Val Pro Glu Gly Ser
 350 355 360

ggc ctg cac tgacccgact ctgatccaga gcgcacaccc gaagcgggag 1336
 Gly Leu His
 365

ccaagggatg ctgaggatct gcgcagagac caccgcgccca ccaagctcgg ctccccgcc 1396
 ccgggaaggt tctcaataaa ggactcaagt gtccc 1431

<210> 2
 <211> 366
 <212> PRT
 <213> Mus musculus

<400> 2
 Met Asn Phe Thr Val Gly Phe Lys Pro Leu Leu Gly Asp Ala His Asn
 1 5 10 15

Met Asp Asn Leu Glu Lys Gln Leu Ile Cys Pro Ile Cys Leu Glu Met
 20 25 30

Phe Ser Lys Pro Val Val Ile Leu Pro Cys Gln His Asn Leu Cys Arg
 35 40 45

Lys Cys Ala Asn Asp Val Phe Gln Ala Ser Asn Pro Leu Trp Gln Ser
 50 55 60

Arg Gly Ser Thr Thr Val Ser Ser Gly Gly Arg Phe Arg Cys Pro Ser
 65 70 75 80

Cys Arg His Glu Val Val Leu Asp Arg His Gly Val Tyr Gly Leu Gln
 85 90 95

Arg Asn Leu Leu Val Glu Asn Ile Ile Asp Ile Tyr Lys Gln Glu Ser
 100 105 110

Ser Arg Pro Leu His Ala Lys Ala Glu Gln His Leu Met Cys Glu Glu
 115 120 125

His Glu Asp Glu Lys Ile Asn Ile Tyr Cys Leu Ser Cys Glu Val Pro
 130 135 140

Thr Cys Ser Leu Cys Lys Val Phe Gly Ala His Lys Asp Cys Glu Val

145	150	155	160
Ala Pro Leu Pro Thr Ile Tyr Lys Arg Gln Lys Ser Glu Leu Ser Asp			
165		170	175
Gly Ile Ala Met Leu Val Ala Gly Asn Asp Arg Val Gln Ala Val Ile			
180	185		190
Thr Gln Met Glu Glu Val Cys Gln Thr Ile Glu Asp Asn Ser Arg Arg			
195	200		205
Gln Lys Gln Leu Leu Asn Gln Arg Phe Glu Thr Leu Cys Ala Val Leu			
210	215	220	
Glu Glu Arg Lys Gly Glu Leu Leu Gln Ala Leu Ala Arg Glu Gln Glu			
225	230	235	240
Glu Lys Leu Gln Arg Val Arg Gly Leu Ile Arg Gln Tyr Gly Asp His			
245	250		255
Leu Glu Gly Ser Ser Lys Leu Val Glu Ser Ala Ile Gln Ser Met Glu			
260	265		270
Glu Pro Gln Met Ala Leu Tyr Leu Gln Gln Ala Lys Glu Leu Ile Asn			
275	280		285
Lys Val Gly Ala Met Ser Lys Val Glu Leu Ala Gly Arg Pro Glu Pro			
290	295	300	
Gly Tyr Glu Ser Met Glu Gln Phe Ser Val Ser Val Glu His Val Ala			
305	310	315	320
Glu Met Leu Arg Thr Ile Asp Phe Gln Pro Gly Ala Ala Gly Asp Glu			
325	330		335
Glu Asp Asp Asp Met Ala Leu Asp Gly Glu Glu Gly Asn Ala Gly Leu			
340	345		350
Glu Glu Glu Arg Leu Asp Val Pro Glu Gly Ser Gly Leu His			
355	360		365

<210> 3

<211> 2590

<212> DNA

<213> Mus musculus

<220>

<221> CDS

<222> (80)..(1714)

<400> 3

ctcgagattt acccttacag aagctgttcg ggagcacctt tcccttgga gcacactcag 60

ggacagggac ggcaaggaa atg agc act tct ctg aat tac aag tct ttc tcc 112
Met Ser Thr Ser Leu Asn Tyr Lys Ser Phe Ser

aaa gag cag cag acc atg gat aac ttg gaa aag caa ctg atc tgt ccc 160
 Lys Glu Gln Gln Thr Met Asp Asn Leu Glu Lys Gln Leu Ile Cys Pro
 15 20 25

atc tgc cta gag atg ttc acg aag cct gtg gtc att ctc cct tgc cag 208
 Ile Cys Leu Glu Met Phe Thr Lys Pro Val Val Ile Leu Pro Cys Gln
 30 35 40

cac aac ctg tgc agg aaa tgt gcc agt gac atc ttc cag gcc tct aac 256
 His Asn Leu Cys Arg Lys Cys Ala Ser Asp Ile Phe Gln Ala Ser Asn
 45 50 55

ccg tac tta ccc aca aga gga ggc acc acc gtg gca tca ggg ggc cgc 304
 Pro Tyr Leu Pro Thr Arg Gly Gly Thr Thr Val Ala Ser Gly Gly Arg
 60 65 70 75

ttc cgc tgt ccc tcc tgc aga cat gag gtg gtg tta gac aga cat ggg 352
 Phe Arg Cys Pro Ser Cys Arg His Glu Val Val Leu Asp Arg His Gly
 80 85 90

gtc tat gga ctg cag agg aac ctg ctc gtg gaa aac att att gat atc 400
 Val Tyr Gly Leu Gln Arg Asn Leu Leu Val Glu Asn Ile Ile Asp Ile
 95 100 105

tac aag cag gaa tcc acc agg cca gaa aaa aaa ttg gac cag ccc atg 448
 Tyr Lys Gln Glu Ser Thr Arg Pro Glu Lys Lys Leu Asp Gln Pro Met
 110 115 120

tgt gaa gag cat gaa gag gaa cgc atc aac atc tat tgt ctg aac tgt 496
 Cys Glu Glu His Glu Glu Glu Arg Ile Asn Ile Tyr Cys Leu Asn Cys
 125 130 135

gaa gtg ccc acc tgt tcc ttg tgc aag gtt ttt ggc gcc cat aag gac 544
 Glu Val Pro Thr Cys Ser Leu Cys Lys Val Phe Gly Ala His Lys Asp
 140 145 150 155

tgc cag gtg gct ccc ctg act cat gtg ttc cag agg cag aag tca gag 592
 Cys Gln Val Ala Pro Leu Thr His Val Phe Gln Arg Gln Lys Ser Glu
 160 165 170

ctc agt gat ggt att gct gta ctt gtg gga agc aac gat aga gtc cag 640
 Leu Ser Asp Gly Ile Ala Val Leu Val Gly Ser Asn Asp Arg Val Gln
 175 180 185

ggt gtg atc agc cag ctg gag gac acc tgt aaa act att gag gag tgc 688
 Gly Val Ile Ser Gln Leu Glu Asp Thr Cys Lys Thr Ile Glu Glu Cys
 190 195 200

tgc aga aag cag aaa cag gac ctg tgt gag aaa ttt gat cac cta tac 736
 Cys Arg Lys Gln Lys Gln Asp Leu Cys Glu Lys Phe Asp His Leu Tyr
 205 210 215

ggc atc ctg gag gag agg aag act gaa atg acc caa gcc atc act cga 784
 Gly Ile Leu Glu Glu Arg Lys Thr Glu Met Thr Gln Ala Ile Thr Arg
 225 230 235

aca cag gag gag aaa ctg gaa cat gtc cga act ctt atc agg aag tat	832
Thr Gln Glu Glu Lys Leu Glu His Val Arg Thr Leu Ile Arg Lys Tyr	
240 245 250	
tcc gat cac ctg gag aac gta tcc aag ttg gtg gag tca gga atc cag	880
Ser Asp His Leu Glu Asn Val Ser Lys Leu Val Glu Ser Gly Ile Gln	
255 260 265	
ttc atg gat gag ccc gaa atg gca gta ttt ctg cag aat gcc aag acc	928
Phe Met Asp Glu Pro Glu Met Ala Val Phe Leu Gln Asn Ala Lys Thr	
270 275 280	
ctg ttg caa aag atc gtg gaa gca tca aag gcg ttt cag atg gag aaa	976
Leu Leu Gln Lys Ile Val Glu Ala Ser Lys Ala Phe Gln Met Glu Lys	
285 290 295	
cta gaa caa ggt tat gag atc atg agc aac ttc act gtc aat ctc aat	1024
Leu Glu Gln Gly Tyr Glu Ile Met Ser Asn Phe Thr Val Asn Leu Asn	
300 305 310 315	
aga gaa gaa aaa att atc cgt gaa att gac ttt tct aga gaa gag gaa	1072
Arg Glu Glu Lys Ile Ile Arg Glu Ile Asp Phe Ser Arg Glu Glu Glu	
320 325 330	
gag gaa gaa gat gca gga gaa ata gat gaa gaa gga gaa gga gag gat	1120
Glu Glu Glu Asp Ala Gly Glu Ile Asp Glu Glu Gly Glu Gly Glu Asp	
335 340 345	
gca gta gaa gta gaa gag gca gaa aat gtt caa ata gca tct tca ggg	1168
Ala Val Glu Val Glu Glu Ala Glu Asn Val Gln Ile Ala Ser Ser Gly	
350 355 360	
gaa gag gag agt ctg gag aaa gct gca gag ccc tct cag ctt ccc gca	1216
Glu Glu Glu Ser Leu Glu Lys Ala Ala Glu Pro Ser Gln Leu Pro Ala	
365 370 375	
gag ctt cag gtc gcc cca gag cca cta cct gct tcc tct cca gaa ccg	1264
Glu Leu Gln Val Ala Pro Glu Pro Leu Pro Ala Ser Ser Pro Glu Pro	
380 385 390 395	
ttt tca tcc atg cca cct gct gca gat gtc ctg gtg aca cag ggg gag	1312
Phe Ser Ser Met Pro Pro Ala Ala Asp Val Leu Val Thr Gln Gly Glu	
400 405 410	
gtg gtg ccc att ggc tct cag cag acc aca cag tct gaa act tca ggc	1360
Val Val Pro Ile Gly Ser Gln Gln Thr Thr Gln Ser Glu Thr Ser Gly	
415 420 425	
cct tca gca gcg gaa act gcg gat ccc ttg ttt tac cct agt tgg tat	1408
Pro Ser Ala Ala Glu Thr Ala Asp Pro Leu Phe Tyr Pro Ser Trp Tyr	
430 435 440	
aaa ggc caa agc cgg aaa acc agc tcc aac cca cct tgc act cat ggg	1456
Lys Gly Gln Ser Arg Lys Thr Ser Ser Asn Pro Pro Cys Thr His Gly	
445 450 455	

agt gaa ggt ctg ggt caa ata ggg cct ctg ggc att gag gat tcc agt 1504
 Ser Glu Gly Leu Gly Gln Ile Gly Pro Leu Gly Ile Glu Asp Ser Ser
 460 465 470 475

gtg cag tcc gca gaa gtg gca gaa gcc gca acc aat gag cag gca gca 1552
 Val Gln Ser Ala Glu Val Ala Glu Ala Ala Thr Asn Glu Gln Ala Ala
 480 485 490

gtg agt ggt aag gag tct agt tca act gca gct acc tct cag att gga 1600
 Val Ser Gly Lys Glu Ser Ser Ser Thr Ala Ala Thr Ser Gln Ile Gly
 495 500 505

ttt gag gcc cct tct ccc cag gga cag tct gca gcc ttg ggg agt ggg 1648
 Phe Glu Ala Pro Ser Pro Gln Gly Gln Ser Ala Ala Leu Gly Ser Gly
 510 515 520

ggt ggg gtg atc ctg agc cag ctc gcc acg tct tct cct tct cct ggt 1696
 Gly Gly Val Ile Leu Ser Gln Leu Ala Thr Ser Ser Pro Ser Pro Gly
 525 530 535

ttg aat tcc cta aat gaa taatatttat tctcgttgct gccccctgtc 1744
 Leu Asn Ser Leu Asn Glu
 540 545

tgccctggctg aaaagcacat aggcagcagg aaacaggtgg aaattcacca cgattcatat 1804
 gaaggggacc tctggacagg atttctgaaa gcaaaacaaa acaatacaac accaccaccc 1864
 ttttaattcca gatgacttat ctcactcatt gagaaaatga ttatgctcag aacaaaatta 1924
 cagaaaatac tcttctgaag aaacttgatc ttctgcaaat ctttcatttg tgtgagaaac 1984
 cttctgaagg ttgtgtaggt gtggtgcatg cctgtgtatc agccataagt gccaaagtgg 2044
 aacaaagtgg cagaacactc tcccagcctc cctcaggctt ctggttattt taggacgctt 2104
 gtgccttttg cttttctcct tagcattgca ggtggttaggt gatgttcagt gtcagttcca 2164
 aactgaccga tttatcaaaa tatggagatt ggtcactgac caaagctatg tagggcactg 2224
 tagaggttcc tttccctatg gatgccatgg gtgcgcagac aggactttcc tttacatgtg 2284
 gccacacgtc catagtccag aaggccaaaa atctagggca actcttttga catttttcta 2344
 accttattta catatctcat aatcatatcc atgtattagg cattttaatt gaatttcaaa 2404
 gaggagctgt ctactttctt aagtgtcctg ccatagcagc aatctgataa tctgtggagc 2464
 aactgcatgg atttaagtat acacacaatt ctccccctgt gtgccttctc tctctctctc 2524
 tctccccctc tctccctctg tctcttctct cccccctgt ctctccctcc tttcctttct 2584
 tcctcc 2590

<210> 4
 <211> 545

<212> PRT

<213> Mus musculus

<400> 4

Met Ser Thr Ser Leu Asn Tyr Lys Ser Phe Ser Lys Glu Gln Gln Thr
1 5 10 15

Met Asp Asn Leu Glu Lys Gln Leu Ile Cys Pro Ile Cys Leu Glu Met
20 25 30

Phe Thr Lys Pro Val Val Ile Leu Pro Cys Gln His Asn Leu Cys Arg
35 40 45

Lys Cys Ala Ser Asp Ile Phe Gln Ala Ser Asn Pro Tyr Leu Pro Thr
50 55 60

Arg Gly Gly Thr Thr Val Ala Ser Gly Gly Arg Phe Arg Cys Pro Ser
65 70 75 80

Cys Arg His Glu Val Val Leu Asp Arg His Gly Val Tyr Gly Leu Gln
85 90 95

Arg Asn Leu Leu Val Glu Asn Ile Ile Asp Ile Tyr Lys Gln Glu Ser
100 105 110

Thr Arg Pro Glu Lys Lys Leu Asp Gln Pro Met Cys Glu Glu His Glu
115 120 125

Glu Glu Arg Ile Asn Ile Tyr Cys Leu Asn Cys Glu Val Pro Thr Cys
130 135 140

Ser Leu Cys Lys Val Phe Gly Ala His Lys Asp Cys Gln Val Ala Pro
145 150 155 160

Leu Thr His Val Phe Gln Arg Gln Lys Ser Glu Leu Ser Asp Gly Ile
165 170 175

Ala Val Leu Val Gly Ser Asn Asp Arg Val Gln Gly Val Ile Ser Gln
180 185 190

Leu Glu Asp Thr Cys Lys Thr Ile Glu Glu Cys Cys Arg Lys Gln Lys
195 200 205

Gln Asp Leu Cys Glu Lys Phe Asp His Leu Tyr Gly Ile Leu Glu Glu
210 215 220

Arg Lys Thr Glu Met Thr Gln Ala Ile Thr Arg Thr Gln Glu Glu Lys
225 230 235 240

Leu Glu His Val Arg Thr Leu Ile Arg Lys Tyr Ser Asp His Leu Glu
245 250 255

Asn Val Ser Lys Leu Val Glu Ser Gly Ile Gln Phe Met Asp Glu Pro
260 265 270

Glu Met Ala Val Phe Leu Gln Asn Ala Lys Thr Leu Leu Gln Lys Ile
275 280 285

Val Glu Ala Ser Lys Ala Phe Gln Met Glu Lys Leu Glu Gln Gly Tyr
 290 295 300
 Glu Ile Met Ser Asn Phe Thr Val Asn Leu Asn Arg Glu Glu Lys Ile
 305 310 315 320
 Ile Arg Glu Ile Asp Phe Ser Arg Glu Glu Glu Glu Glu Asp Ala
 325 330 335
 Gly Glu Ile Asp Glu Glu Gly Glu Gly Glu Asp Ala Val Glu Val Glu
 340 345 350
 Glu Ala Glu Asn Val Gln Ile Ala Ser Ser Gly Glu Glu Glu Ser Leu
 355 360 365
 Glu Lys Ala Ala Glu Pro Ser Gln Leu Pro Ala Glu Leu Gln Val Ala
 370 375 380
 Pro Glu Pro Leu Pro Ala Ser Ser Pro Glu Pro Phe Ser Ser Met Pro
 385 390 395 400
 Pro Ala Ala Asp Val Leu Val Thr Gln Gly Glu Val Val Pro Ile Gly
 405 410 415
 Ser Gln Gln Thr Thr Gln Ser Glu Thr Ser Gly Pro Ser Ala Ala Glu
 420 425 430
 Thr Ala Asp Pro Leu Phe Tyr Pro Ser Trp Tyr Lys Gly Gln Ser Arg
 435 440 445
 Lys Thr Ser Ser Asn Pro Pro Cys Thr His Gly Ser Glu Gly Leu Gly
 450 455 460
 Gln Ile Gly Pro Leu Gly Ile Glu Asp Ser Ser Val Gln Ser Ala Glu
 465 470 475 480
 Val Ala Glu Ala Ala Thr Asn Glu Gln Ala Ala Val Ser Gly Lys Glu
 485 490 495
 Ser Ser Ser Thr Ala Ala Thr Ser Gln Ile Gly Phe Glu Ala Pro Ser
 500 505 510
 Pro Gln Gly Gln Ser Ala Ala Leu Gly Ser Gly Gly Gly Val Ile Leu
 515 520 525
 Ser Gln Leu Ala Thr Ser Ser Pro Ser Pro Gly Leu Asn Ser Leu Asn
 530 535 540
 Glu
 545

<210> 5
 <211> 1597
 <212> DNA

<213> Mus musculus

<220>

<221> CDS

<222> (299)..(1327)

<400> 5

```
ctcgagatTT acccttacag aagctgttcg ggagcacctt tcccttggca gcacactcag 60
ggacagggac ggcaaggaaa tgagcacttc tctgaattac aagtctttct ccaaagagca 120
gcagaccatg gataacttgg aaaagcaact gatctgtccc atctgcctag agatgttcac 180
gaagcctgtg gtcattctcc cttgccagca caacctgtgc aggaaatgtg cgggcccccc 240
ttggagacaa agacttggtg tgacgcaggt gggcaagaca gtcgcatttc aaagcaat 298
atg gat tat aaa tct agc ctg att cct gat gga aac gct atg gag aac 346
Met Asp Tyr Lys Ser Ser Leu Ile Pro Asp Gly Asn Ala Met Glu Asn
  1           5           10          15
ctg gag aag cag ctg atc tgc ccc atc tgc ctg gag atg ttt acc aag 394
Leu Glu Lys Gln Leu Ile Cys Pro Ile Cys Leu Glu Met Phe Thr Lys
      20           25           30
cct gtg gtc atc ctg ccc tgc caa cac aac ctc tgc cgg aag tgt gcc 442
Pro Val Val Ile Leu Pro Cys Gln His Asn Leu Cys Arg Lys Cys Ala
      35           40           45
aac gac atc ttc cag gct gcg aat ccc tac tgg acc aac cgc ggt ggc 490
Asn Asp Ile Phe Gln Ala Ala Asn Pro Tyr Trp Thr Asn Arg Gly Gly
      50           55           60
tca gtg tcc atg tct gga ggt cgt ttc cgt tgc ccc tcg tgc cgc cat 538
Ser Val Ser Met Ser Gly Gly Arg Phe Arg Cys Pro Ser Cys Arg His
      65           70           75           80
gaa gtg atc atg gac cgg cac ggg gtg tac ggc ctg cag agg aac ctg 586
Glu Val Ile Met Asp Arg His Gly Val Tyr Gly Leu Gln Arg Asn Leu
      85           90           95
ctg gtg gaa aac atc att gac atc tac aag cag gag tgc tcc agt cgg 634
Leu Val Glu Asn Ile Ile Asp Ile Tyr Lys Gln Glu Cys Ser Ser Arg
      100          105          110
ccc ctg cag aaa ggc agc cac ccg atg tgc aag gaa cac gaa gac gag 682
Pro Leu Gln Lys Gly Ser His Pro Met Cys Lys Glu His Glu Asp Glu
      115          120          125
aag atc aac atc tac tgt ctc acg tgt gag gtg cct act tgc tcc ttg 730
Lys Ile Asn Ile Tyr Cys Leu Thr Cys Glu Val Pro Thr Cys Ser Leu
      130          135          140
tgc aag gtg ttt ggg gct cac cag gcc tgt gag gtt gcc cct ttg caa 778
Cys Lys Val Phe Gly Ala His Gln Ala Cys Glu Val Ala Pro Leu Gln
      145          150          155          160
```

agc atc ttc caa gga cag aag act gag ctg agt aac tgc atc tcc atg	826
Ser Ile Phe Gln Gly Gln Lys Thr Glu Leu Ser Asn Cys Ile Ser Met	
165 170 175	
ctg gtg gcg ggg aac gac cga gtg cag acg atc atc tct cag ctg gag	874
Leu Val Ala Gly Asn Asp Arg Val Gln Thr Ile Ile Ser Gln Leu Glu	
180 185 190	
gac tcg tgc aga gtg acc aag gag aat agc cac cag gtg aag gag gag	922
Asp Ser Cys Arg Val Thr Lys Glu Asn Ser His Gln Val Lys Glu Glu	
195 200 205	
ctg agt cag aag ttt gac acc ctc tac gcc atc ctg gat gag aag aag	970
Leu Ser Gln Lys Phe Asp Thr Leu Tyr Ala Ile Leu Asp Glu Lys Lys	
210 215 220	
agc gag ctg ctg cag cgg atc acg cag gag cag gag gag aag ctg ggc	1018
Ser Glu Leu Leu Gln Arg Ile Thr Gln Glu Gln Glu Glu Lys Leu Gly	
225 230 235 240	
ttc atc gag gct ctg atc ctc cag tac agg gag cag ctg gaa aag tcc	1066
Phe Ile Glu Ala Leu Ile Leu Gln Tyr Arg Glu Gln Leu Glu Lys Ser	
245 250 255	
acc aag ctt gtg gag acc gcc atc cag tcc ctg gat gag ccc gga ggg	1114
Thr Lys Leu Val Glu Thr Ala Ile Gln Ser Leu Asp Glu Pro Gly Gly	
260 265 270	
gct acc ttc ctc tca agt gcc aag cag ctc atc aag agc att gta gaa	1162
Ala Thr Phe Leu Ser Ser Ala Lys Gln Leu Ile Lys Ser Ile Val Glu	
275 280 285	
gcc tcc aag ggc tgc cag ctg ggg aag aca gag caa ggc ttt gag aac	1210
Ala Ser Lys Gly Cys Gln Leu Gly Lys Thr Glu Gln Gly Phe Glu Asn	
290 295 300	
atg gac tac ttt act ctg gac tta gaa cac ata gca gag gcc ttg agg	1258
Met Asp Tyr Phe Thr Leu Asp Leu Glu His Ile Ala Glu Ala Leu Arg	
305 310 315 320	
gcc att gac ttt ggg aca ggt aaa gga tgt gat gtt aca tgt ttg acc	1306
Ala Ile Asp Phe Gly Thr Gly Lys Gly Cys Asp Val Thr Cys Leu Thr	
325 330 335	
ttt gaa agg cag cgt tcc tct tgagttctga ggggaactgt taaaaaagtc	1357
Phe Glu Arg Gln Arg Ser Ser	
340	
aaatttacac agccagtgtt gacaggtctc tctatggagc cctgactgtc ttagtagtgt	1417
ctaagtagac caagctggtc tggaacacat agagatctat cttgcccatc tctgcttctt	1477
gagggatgag ataaaaggca tgtgccacc atgcctggct ccacagacaa ctttgtgatg	1537
gatccagggc ctggcacagt gcctgggtaca taattgtttc gaaataaatt atctcgtgcc	1597

<210> 6
<211> 343
<212> PRT
<213> Mus musculus

<400> 6

Met	Asp	Tyr	Lys	Ser	Ser	Leu	Ile	Pro	Asp	Gly	Asn	Ala	Met	Glu	Asn	
1				5					10					15		
Leu	Glu	Lys	Gln	Leu	Ile	Cys	Pro	Ile	Cys	Leu	Glu	Met	Phe	Thr	Lys	
			20					25					30			
Pro	Val	Val	Ile	Leu	Pro	Cys	Gln	His	Asn	Leu	Cys	Arg	Lys	Cys	Ala	
		35					40					45				
Asn	Asp	Ile	Phe	Gln	Ala	Ala	Asn	Pro	Tyr	Trp	Thr	Asn	Arg	Gly	Gly	
	50					55					60					
Ser	Val	Ser	Met	Ser	Gly	Gly	Arg	Phe	Arg	Cys	Pro	Ser	Cys	Arg	His	
65					70					75					80	
Glu	Val	Ile	Met	Asp	Arg	His	Gly	Val	Tyr	Gly	Leu	Gln	Arg	Asn	Leu	
				85					90					95		
Leu	Val	Glu	Asn	Ile	Ile	Asp	Ile	Tyr	Lys	Gln	Glu	Cys	Ser	Ser	Arg	
			100					105					110			
Pro	Leu	Gln	Lys	Gly	Ser	His	Pro	Met	Cys	Lys	Glu	His	Glu	Asp	Glu	
		115					120					125				
Lys	Ile	Asn	Ile	Tyr	Cys	Leu	Thr	Cys	Glu	Val	Pro	Thr	Cys	Ser	Leu	
	130					135					140					
Cys	Lys	Val	Phe	Gly	Ala	His	Gln	Ala	Cys	Glu	Val	Ala	Pro	Leu	Gln	
145					150					155					160	
Ser	Ile	Phe	Gln	Gly	Gln	Lys	Thr	Glu	Leu	Ser	Asn	Cys	Ile	Ser	Met	
			165						170						175	
Leu	Val	Ala	Gly	Asn	Asp	Arg	Val	Gln	Thr	Ile	Ile	Ser	Gln	Leu	Glu	
		180						185					190			
Asp	Ser	Cys	Arg	Val	Thr	Lys	Glu	Asn	Ser	His	Gln	Val	Lys	Glu	Glu	
		195					200					205				
Leu	Ser	Gln	Lys	Phe	Asp	Thr	Leu	Tyr	Ala	Ile	Leu	Asp	Glu	Lys	Lys	
	210					215					220					
Ser	Glu	Leu	Leu	Gln	Arg	Ile	Thr	Gln	Glu	Gln	Glu	Glu	Lys	Leu	Gly	
225					230				235						240	
Phe	Ile	Glu	Ala	Leu	Ile	Leu	Gln	Tyr	Arg	Glu	Gln	Leu	Glu	Lys	Ser	
			245						250					255		
Thr	Lys	Leu	Val	Glu	Thr	Ala	Ile	Gln	Ser	Leu	Asp	Glu	Pro	Gly	Gly	
		260						265					270			

Ala Thr Phe Leu Ser Ser Ala Lys Gln Leu Ile Lys Ser Ile Val Glu
275 280 285

Ala Ser Lys Gly Cys Gln Leu Gly Lys Thr Glu Gln Gly Phe Glu Asn
290 295 300

Met Asp Tyr Phe Thr Leu Asp Leu Glu His Ile Ala Glu Ala Leu Arg
305 310 315 320

Ala Ile Asp Phe Gly Thr Gly Lys Gly Cys Asp Val Thr Cys Leu Thr
325 330 335

Phe Glu Arg Gln Arg Ser Ser
340